

DX01074 Seq Listing.ST25  
SEQUENCE LISTING

<110> Chirica, Madaline

Parham, Christi L.

Kastelein, Robert A.

Moore, Kevin W.

<120> Mammalian Receptor Proteins; Related Reagents and Methods.

<130> DX01074

<140> 09/853,180

<141> 2001-05-10

<150> 60/203,426

<151> 2000-05-10

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 2859

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119)..(2005)

<223>

<400> 1

## DX01074 Seq Listing.ST25

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ggaattatgt gcttcaaaca gggtgaaaga gggaaacagt cttttcctgc ttccagac	118
atg aat cak gtc act att caa tgg gat gca gta ata gcc ctt tac ata Met Asn Xaa Val Thr Ile Gln Trp Asp Ala Val Ile Ala Leu Tyr Ile 1 5 10 15	166
ctc ttc agc tgg tgt cat gga gga att aca aat ata aac tgc tct ggc Leu Phe Ser Trp Cys His Gly Gly Ile Thr Asn Ile Asn Cys Ser Gly 20 25 30	214
cac atc tgg gta gaa cca gcc aca att ttt aag atg ggt atg aat atc His Ile Trp Val Glu Pro Ala Thr Ile Phe Lys Met Gly Met Asn Ile 35 40 45	262
tct ata tat tgc caa gca gca att aag aac tgc caa cca agg aaa ctt Ser Ile Tyr Cys Gln Ala Ala Ile Lys Asn Cys Gln Pro Arg Lys Leu 50 55 60	310
cat ttt tat aaa aat ggc atc aaa gaa aga ttt caa atc aca agg att His Phe Tyr Lys Asn Gly Ile Lys Glu Arg Phe Gln Ile Thr Arg Ile 65 70 75 80	358
aat aaa aca aca gct cgg ctt tgg tat aaa aac ttt ctg gaa cca cat Asn Lys Thr Thr Ala Arg Leu Trp Tyr Lys Asn Phe Leu Glu Pro His 85 90 95	406
gct tct atg tac tgc act gct gaa tgt ccc aaa cat ttt caa gag aca Ala Ser Met Tyr Cys Thr Ala Glu Cys Pro Lys His Phe Gln Glu Thr 100 105 110	454
ctg ata tgt gga aaa gac att tct tct gga tat ccg cca gat att cct Leu Ile Cys Gly Lys Asp Ile Ser Ser Gly Tyr Pro Pro Asp Ile Pro 115 120 125	502
gat gaa gta acc tgt gtc att tat gaa tat tca ggc aac atg act tgc Asp Glu Val Thr Cys Val Ile Tyr Glu Tyr Ser Gly Asn Met Thr Cys 130 135 140	550
acc tgg aat gct rgg aag ctc acc tac ata gac aca aaa tac gtg gta Thr Trp Asn Ala Xaa Lys Leu Thr Tyr Ile Asp Thr Lys Tyr Val Val 145 150 155 160	598
cat gtg aag agt tta gag aca gaa gaa gag caa cag tat ctc acc tca His Val Lys Ser Leu Glu Thr Glu Glu Glu Gln Gln Tyr Leu Thr Ser 165 170 175	646
agc tat att aac atc tcc act gat tca tta caa ggt ggc aag aag tac Ser Tyr Ile Asn Ile Ser Thr Asp Ser Leu Gln Gly Gly Lys Lys Tyr 180 185 190	694
ttg gtt tgg gtc caa gca gca aac gca cta ggc atg gaa gag tca aaa Leu Val Trp Val Gln Ala Ala Asn Ala Leu Gly Met Glu Glu Ser Lys 195 200 205	742
caa ctg caa att cac ctg gat gat ata gtg ata cct tct gca gcc gtc Gln Leu Gln Ile His Leu Asp Asp Ile Val Ile Pro Ser Ala Ala Val 210 215 220	790
att tcc agg gct gag act ata aat gct aca gtg ccc aag acc ata att Ile Ser Arg Ala Glu Thr Ile Asn Ala Thr Val Pro Lys Thr Ile Ile 225 230 235 240	838

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tat tgg gat agt caa aca aca att gaa aag gtt tcc tgt gaa atg aga Tyr Trp Asp Ser Gln Thr Thr Ile Glu Lys Val Ser Cys Glu Met Arg 245 250 255	886
tac aag gct aca aca aac caa act tgg aat gtt aaa gaa ttt gac acc Tyr Lys Ala Thr Thr Asn Gln Thr Trp Asn Val Lys Glu Phe Asp Thr 260 265 270	934
aat ttt aca tat gtg caa cag tca gaa ttc tac ttg gag cca aac att Asn Phe Thr Tyr Val Gln Gln Ser Glu Phe Tyr Leu Glu Pro Asn Ile 275 280 285	982
aag tac gta ttt caa gtg aga tgt caa gaa aca ggc aaa agg tac tgg Lys Tyr Val Phe Gln Val Arg Cys Gln Glu Thr Gly Lys Arg Tyr Trp 290 295 300	1030
cag cct tgg agt tca ccg ttt ttt cat aaa aca cct gaa aca gtt ccc Gln Pro Trp Ser Ser Pro Phe Phe His Lys Thr Pro Glu Thr Val Pro 305 310 315 320	1078
cag gtc aca tca aaa gca ttc caa cat gac aca tgg aat tct ggg cta Gln Val Thr Ser Lys Ala Phe Gln His Asp Thr Trp Asn Ser Gly Leu 325 330 335	1126
aca gtt gct tcc atc tct aca ggg cac ctt act tct gac aac aga gga Thr Val Ala Ser Ile Ser Thr Gly His Leu Thr Ser Asp Asn Arg Gly 340 345 350	1174
gac att gga ctt tta ttg gga atg atc gtc ttt gct gtt atg ttg tca Asp Ile Gly Leu Leu Leu Gly Met Ile Val Phe Ala Val Met Leu Ser 355 360 365	1222
att ctt tct ttg att ggg ata ttt aac aga tca ttc cga act ggg att Ile Leu Ser Leu Ile Gly Ile Phe Asn Arg Ser Phe Arg Thr Gly Ile 370 375 380	1270
aaa aga agg atc tta ttg tta ata cca aag tgg ctt tat gaa gat att Lys Arg Arg Ile Leu Leu Leu Ile Pro Lys Trp Leu Tyr Glu Asp Ile 385 390 395 400	1318
cct aat atg aaa aac agc aat gtt gtg aaa atg cta cag gaa aat agt Pro Asn Met Lys Asn Ser Asn Val Val Lys Met Leu Gln Glu Asn Ser 405 410 415	1366
gaa ctt atg aat aat aat tcc agt gag cag gtc cta tat gtt gat ccc Glu Leu Met Asn Asn Asn Ser Ser Glu Gln Val Leu Tyr Val Asp Pro 420 425 430	1414
atg att aca gag ata aaa gaa atc ttc atc cca gaa cac aag cct aca Met Ile Thr Glu Ile Lys Glu Ile Phe Ile Pro Glu His Lys Pro Thr 435 440 445	1462
gac tac aag aag gag aat aca gga ccc ctg gag aca aga gac tac ccg Asp Tyr Lys Lys Glu Asn Thr Gly Pro Leu Glu Thr Arg Asp Tyr Pro 450 455 460	1510
caa aac tcg cta ttc gac aat act aca gtt gta tat att cct gat ctc Gln Asn Ser Leu Phe Asp Asn Thr Thr Val Val Tyr Ile Pro Asp Leu 465 470 475 480	1558
aac act gga tat aaa ccc caa att tca aat ttt ctg cct gag gga agc Asn Thr Gly Tyr Lys Pro Gln Ile Ser Asn Phe Leu Pro Glu Gly Ser 485 490 495	1606

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485

490

495

cat ctc agc aat aat aat gaa att act tcc tta aca ctt aaa cca cca	1654
His Leu Ser Asn Asn Asn Glu Ile Thr Ser Leu Thr Leu Lys Pro Pro	
500 505 510	
ggt gat tcc tta gac tca gga aat aat ccc agg tta caa aag cat cct	1702
Val Asp Ser Leu Asp Ser Gly Asn Asn Pro Arg Leu Gln Lys His Pro	
515 520 525	
aat ttt gct ttt tct gtt tca agt gtg aat tca cta agc aac aca ata	1750
Asn Phe Ala Phe Ser Val Ser Ser Val Asn Ser Leu Ser Asn Thr Ile	
530 535 540	
ttt ctt gga gaa tta agc ctc ata tta aat caa gga gaa tgc agt tct	1798
Phe Leu Gly Glu Leu Ser Leu Ile Leu Asn Gln Gly Glu Cys Ser Ser	
545 550 555 560	
cct gac ata caa aac tca gta gag gag gaa acc acc atg ctt ttg gaa	1846
Pro Asp Ile Gln Asn Ser Val Glu Glu Glu Thr Thr Met Leu Leu Glu	
565 570 575	
aat gat tca ccc agt gaa act att cca gaa cag acc ctg ctt cct gat	1894
Asn Asp Ser Pro Ser Glu Thr Ile Pro Glu Gln Thr Leu Leu Pro Asp	
580 585 590	
gaa ttt gtc tcc tgt ttg ggg atc gtg aat gag gag ttg cca tct att	1942
Glu Phe Val Ser Cys Leu Gly Ile Val Asn Glu Glu Leu Pro Ser Ile	
595 600 605	
aat act tat ttt cca caa aat att ttg gaa agc cac ttc aat agg att	1990
Asn Thr Tyr Phe Pro Gln Asn Ile Leu Glu Ser His Phe Asn Arg Ile	
610 615 620	
tca ctc ttg gaa aag tagagctgtg tgggtcaaaat caatatgaga aagctgcctt	2045
Ser Leu Leu Glu Lys	
625	
gcaatctgaa cttgggtttt ccctgcaata gaaattgaat tctgcctctt tttgaaaaa	2105
atgtattcac atacaaatct tcacatggac acatgttttc atttcccttg gataaatacc	2165
taggtagggg attgctgggc catatgataa gcatatgttt cagttctacc aatcttgttt	2225
ccagagtagt gacatttctg tgctcctacc atcaccatgt aagaattccc gggagctcca	2285
tgctttttta atttttagcca ttcttctgcc tmattttctta aaattagaga attaagggtcc	2345
cgaagggtgga acatgcttca tgggtcacaca tacaggcaca aaaacagcat tatgtggacg	2405
cctcatgtat tttttataga gtcaactatt tcctctttat tttccctcat tgaaagatgc	2465
aaaacagctc tctattgtgt acagaaaggg taaataatgc aaaatacctg gtagtaaat	2525
aaatgctgaa aattttcctt taaaatagaa tcattaggcc aggcgtggtg gctcatgctt	2585
gtaatcccag cactttggta ggctgaggtr ggtggatcac ctgaggtcag gagttcgagt	2645
ccagcctggc caatatgctg aaaccctgtc tctactaaaa ttacaaaaat tagccggcca	2705
tgggtggcagg tgcttgtaat cccagctact tgggaggctg aggcaggaga atcacttgaa	2765
ccaggaaggc agaggttgca ctgagctgag attgtgccac tgcactccag cctgggcaac	2825

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aagagcaaaa ctctgtctgg aaaaaaaaaa aaaa

2859

&lt;210&gt; 2

&lt;211&gt; 629

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (3)..(3)

&lt;223&gt; The 'Xaa' at location 3 stands for Gln, or His.

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (149)..(149)

&lt;223&gt; The 'Xaa' at location 149 stands for Gly, or Arg.

&lt;400&gt; 2

Met Asn Xaa Val Thr Ile Gln Trp Asp Ala Val Ile Ala Leu Tyr Ile  
 1 5 10 15

Leu Phe Ser Trp Cys His Gly Gly Ile Thr Asn Ile Asn Cys Ser Gly  
 20 25 30

His Ile Trp Val Glu Pro Ala Thr Ile Phe Lys Met Gly Met Asn Ile  
 35 40 45

Ser Ile Tyr Cys Gln Ala Ala Ile Lys Asn Cys Gln Pro Arg Lys Leu  
 50 55 60

His Phe Tyr Lys Asn Gly Ile Lys Glu Arg Phe Gln Ile Thr Arg Ile  
 65 70 75 80

Asn Lys Thr Thr Ala Arg Leu Trp Tyr Lys Asn Phe Leu Glu Pro His  
 85 90 95

Ala Ser Met Tyr Cys Thr Ala Glu Cys Pro Lys His Phe Gln Glu Thr  
 100 105 110

Leu Ile Cys Gly Lys Asp Ile Ser Ser Gly Tyr Pro Pro Asp Ile Pro  
 115 120 125

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Asp Glu Val Thr Cys Val Ile Tyr Glu Tyr Ser Gly Asn Met Thr Cys  
 130 135 140

Thr Trp Asn Ala Xaa Lys Leu Thr Tyr Ile Asp Thr Lys Tyr Val Val  
 145 150 155 160

His Val Lys Ser Leu Glu Thr Glu Glu Glu Gln Gln Tyr Leu Thr Ser  
 165 170 175

Ser Tyr Ile Asn Ile Ser Thr Asp Ser Leu Gln Gly Gly Lys Lys Tyr  
 180 185 190

Leu Val Trp Val Gln Ala Ala Asn Ala Leu Gly Met Glu Glu Ser Lys  
 195 200 205

Gln Leu Gln Ile His Leu Asp Asp Ile Val Ile Pro Ser Ala Ala Val  
 210 215 220

Ile Ser Arg Ala Glu Thr Ile Asn Ala Thr Val Pro Lys Thr Ile Ile  
 225 230 235 240

Tyr Trp Asp Ser Gln Thr Thr Ile Glu Lys Val Ser Cys Glu Met Arg  
 245 250 255

Tyr Lys Ala Thr Thr Asn Gln Thr Trp Asn Val Lys Glu Phe Asp Thr  
 260 265 270

Asn Phe Thr Tyr Val Gln Gln Ser Glu Phe Tyr Leu Glu Pro Asn Ile  
 275 280 285

Lys Tyr Val Phe Gln Val Arg Cys Gln Glu Thr Gly Lys Arg Tyr Trp  
 290 295 300

Gln Pro Trp Ser Ser Pro Phe Phe His Lys Thr Pro Glu Thr Val Pro  
 305 310 315 320

Gln Val Thr Ser Lys Ala Phe Gln His Asp Thr Trp Asn Ser Gly Leu  
 325 330 335

Thr Val Ala Ser Ile Ser Thr Gly His Leu Thr Ser Asp Asn Arg Gly  
 340 345 350

Asp Ile Gly Leu Leu Leu Gly Met Ile Val Phe Ala Val Met Leu Ser  
 355 360 365

Ile Leu Ser Leu Ile Gly Ile Phe Asn Arg Ser Phe Arg Thr Gly Ile  
 370 375 380

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Lys Arg Arg Ile Leu Leu Leu Ile Pro Lys Trp Leu Tyr Glu Asp Ile  
385 390 395 400

Pro Asn Met Lys Asn Ser Asn Val Val Lys Met Leu Gln Glu Asn Ser  
405 410 415

Glu Leu Met Asn Asn Asn Ser Ser Glu Gln Val Leu Tyr Val Asp Pro  
420 425 430

Met Ile Thr Glu Ile Lys Glu Ile Phe Ile Pro Glu His Lys Pro Thr  
435 440 445

Asp Tyr Lys Lys Glu Asn Thr Gly Pro Leu Glu Thr Arg Asp Tyr Pro  
450 455 460

Gln Asn Ser Leu Phe Asp Asn Thr Thr Val Val Tyr Ile Pro Asp Leu  
465 470 475 480

Asn Thr Gly Tyr Lys Pro Gln Ile Ser Asn Phe Leu Pro Glu Gly Ser  
485 490 495

His Leu Ser Asn Asn Asn Glu Ile Thr Ser Leu Thr Leu Lys Pro Pro  
500 505 510

Val Asp Ser Leu Asp Ser Gly Asn Asn Pro Arg Leu Gln Lys His Pro  
515 520 525

Asn Phe Ala Phe Ser Val Ser Ser Val Asn Ser Leu Ser Asn Thr Ile  
530 535 540

Phe Leu Gly Glu Leu Ser Leu Ile Leu Asn Gln Gly Glu Cys Ser Ser  
545 550 555 560

Pro Asp Ile Gln Asn Ser Val Glu Glu Glu Thr Thr Met Leu Leu Glu  
565 570 575

Asn Asp Ser Pro Ser Glu Thr Ile Pro Glu Gln Thr Leu Leu Pro Asp  
580 585 590

Glu Phe Val Ser Cys Leu Gly Ile Val Asn Glu Glu Leu Pro Ser Ile  
595 600 605

Asn Thr Tyr Phe Pro Gln Asn Ile Leu Glu Ser His Phe Asn Arg Ile  
610 615 620

Ser Leu Leu Glu Lys

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625

&lt;210&gt; 3

&lt;211&gt; 918

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

Met Leu Thr Leu Gln Thr Trp Val Val Gln Ala Leu Phe Ile Phe Leu  
 1 5 10 15

Thr Thr Glu Ser Thr Gly Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser  
 20 25 30

Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys  
 35 40 45

Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr  
 50 55 60

Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr  
 65 70 75 80

Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser  
 85 90 95

Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu  
 100 105 110

Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys  
 115 120 125

Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys  
 130 135 140

Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu  
 145 150 155 160

Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg  
 165 170 175

Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val  
 180 185 190



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Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr  
195 200 205

Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro  
210 215 220

Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu  
225 230 235 240

Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys  
245 250 255

Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile  
260 265 270

Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp  
275 280 285

Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu  
290 295 300

Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile  
305 310 315 320

Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile  
325 330 335

Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln Leu Val Trp Lys  
340 345 350

Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val  
355 360 365

Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr Thr Val Asn Ala  
370 375 380

Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr Leu Ala Thr Leu  
385 390 395 400

Thr Val Arg Asn Leu Val Gly Lys Ser Asp Ala Ala Val Leu Thr Ile  
405 410 415

Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met Asp Leu Lys Ala  
420 425 430

Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg Glu  
435 440 445

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Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu Ser Asp Lys Ala  
450 455 460

Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr Val His Arg Thr  
465 470 475 480

Tyr Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr Leu Ile Thr Val  
485 490 495

Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala  
500 505 510

Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr Val Arg Thr Lys  
515 520 525

Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp Gln Leu Pro Val  
530 535 540

Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr  
545 550 555 560

Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser Ser His Thr Glu  
565 570 575

Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr Met Val Arg Met  
580 585 590

Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe  
595 600 605

Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ala Ile Val Val Pro  
610 615 620

Val Cys Leu Ala Phe Leu Leu Thr Thr Leu Leu Gly Val Leu Phe Cys  
625 630 635 640

Phe Asn Lys Arg Asp Leu Ile Lys Lys His Ile Trp Pro Asn Val Pro  
645 650 655

Asp Pro Ser Lys Ser His Ile Ala Gln Trp Ser Pro His Thr Pro Pro  
660 665 670

Arg His Asn Phe Asn Ser Lys Asp Gln Met Tyr Ser Asp Gly Asn Phe  
675 680 685

Thr Asp Val Ser Val Val Glu Ile Glu Ala Asn Asp Lys Lys Pro Phe  
690 695 700

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Pro Glu Asp Leu Lys Ser Leu Asp Leu Phe Lys Lys Glu Lys Ile Asn  
705 710 715 720

Thr Glu Gly His Ser Ser Gly Ile Gly Gly Ser Ser Cys Met Ser Ser  
725 730 735

Ser Arg Pro Ser Ile Ser Ser Ser Asp Glu Asn Glu Ser Ser Gln Asn  
740 745 750

Thr Ser Ser Thr Val Gln Tyr Ser Thr Val Val His Ser Gly Tyr Arg  
755 760 765

His Gln Val Pro Ser Val Gln Val Phe Ser Arg Ser Glu Ser Thr Gln  
770 775 780

Pro Leu Leu Asp Ser Glu Glu Arg Pro Glu Asp Leu Gln Leu Val Asp  
785 790 795 800

His Val Asp Gly Gly Asp Gly Ile Leu Pro Arg Gln Gln Tyr Phe Lys  
805 810 815

Gln Asn Cys Ser Gln His Glu Ser Ser Pro Asp Ile Ser His Phe Glu  
820 825 830

Arg Ser Lys Gln Val Ser Ser Val Asn Glu Glu Asp Phe Val Arg Leu  
835 840 845

Lys Gln Gln Ile Ser Asp His Ile Ser Gln Ser Cys Gly Ser Gly Gln  
850 855 860

Met Lys Met Phe Gln Glu Val Ser Ala Ala Asp Ala Phe Gly Pro Gly  
865 870 875 880

Thr Glu Gly Gln Val Glu Arg Phe Glu Thr Val Gly Met Glu Ala Ala  
885 890 895

Thr Asp Glu Gly Met Pro Lys Ser Tyr Leu Pro Gln Thr Val Arg Gln  
900 905 910

Gly Gly Tyr Met Pro Gln  
915

<210> 4

<211> 862

<212> PRT

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&lt;213&gt; Homo sapiens

&lt;400&gt; 4

Met Ala His Thr Phe Arg Gly Cys Ser Leu Ala Phe Met Phe Ile Ile  
 1 5 10 15

Thr Trp Leu Leu Ile Lys Ala Lys Ile Asp Ala Cys Lys Arg Gly Asp  
 20 25 30

Val Thr Val Lys Pro Ser His Val Ile Leu Leu Gly Ser Thr Val Asn  
 35 40 45

Ile Thr Cys Ser Leu Lys Pro Arg Gln Gly Cys Phe His Tyr Ser Arg  
 50 55 60

Arg Asn Lys Leu Ile Leu Tyr Lys Phe Asp Arg Arg Ile Asn Phe His  
 65 70 75 80

His Gly His Ser Leu Asn Ser Gln Val Thr Gly Leu Pro Leu Gly Thr  
 85 90 95

Thr Leu Phe Val Cys Lys Leu Ala Cys Ile Asn Ser Asp Glu Ile Gln  
 100 105 110

Ile Cys Gly Ala Glu Ile Phe Val Gly Val Ala Pro Glu Gln Pro Gln  
 115 120 125

Asn Leu Ser Cys Ile Gln Lys Gly Glu Gln Gly Thr Val Ala Cys Thr  
 130 135 140

Trp Glu Arg Gly Arg Asp Thr His Leu Tyr Thr Glu Tyr Thr Leu Gln  
 145 150 155 160

Leu Ser Gly Pro Lys Asn Leu Thr Trp Gln Lys Gln Cys Lys Asp Ile  
 165 170 175

Tyr Cys Asp Tyr Leu Asp Phe Gly Ile Asn Leu Thr Pro Glu Ser Pro  
 180 185 190

Glu Ser Asn Phe Thr Ala Lys Val Thr Ala Val Asn Ser Leu Gly Ser  
 195 200 205

Ser Ser Ser Leu Pro Ser Thr Phe Thr Phe Leu Asp Ile Val Arg Pro  
 210 215 220

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Leu Pro Pro Trp Asp Ile Arg Ile Lys Phe Gln Lys Ala Ser Val Ser  
 225 230 235 240  
 Arg Cys Thr Leu Tyr Trp Arg Asp Glu Gly Leu Val Leu Leu Asn Arg  
 245 250 255  
 Leu Arg Tyr Arg Pro Ser Asn Ser Arg Leu Trp Asn Met Val Asn Val  
 260 265 270  
 Thr Lys Ala Lys Gly Arg His Asp Leu Leu Asp Leu Lys Pro Phe Thr  
 275 280 285  
 Glu Tyr Glu Phe Gln Ile Ser Ser Lys Leu His Leu Tyr Lys Gly Ser  
 290 295 300  
 Trp Ser Asp Trp Ser Glu Ser Leu Arg Ala Gln Thr Pro Glu Glu Glu  
 305 310 315 320  
 Pro Thr Gly Met Leu Asp Val Trp Tyr Met Lys Arg His Ile Asp Tyr  
 325 330 335  
 Ser Arg Gln Gln Ile Ser Leu Phe Trp Lys Asn Leu Ser Val Ser Glu  
 340 345 350  
 Ala Arg Gly Lys Ile Leu His Tyr Gln Val Thr Leu Gln Glu Leu Thr  
 355 360 365  
 Gly Gly Lys Ala Met Thr Gln Asn Ile Thr Gly His Thr Ser Trp Thr  
 370 375 380  
 Thr Val Ile Pro Arg Thr Gly Asn Trp Ala Val Ala Val Ser Ala Ala  
 385 390 395 400  
 Asn Ser Lys Gly Ser Ser Leu Pro Thr Arg Ile Asn Ile Met Asn Leu  
 405 410 415  
 Cys Glu Ala Gly Leu Leu Ala Pro Arg Gln Val Ser Ala Asn Ser Glu  
 420 425 430  
 Gly Met Asp Asn Ile Leu Val Thr Trp Gln Pro Pro Arg Lys Asp Pro  
 435 440 445  
 Ser Ala Val Gln Glu Tyr Val Val Glu Trp Arg Glu Leu His Pro Gly  
 450 455 460  
 Gly Asp Thr Gln Val Pro Leu Asn Trp Leu Arg Ser Arg Pro Tyr Asn  
 465 470 475 480

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Val Ser Ala Leu Ile Ser Glu Asn Ile Lys Ser Tyr Ile Cys Tyr Glu  
 485 490 495  
 Ile Arg Val Tyr Ala Leu Ser Gly Asp Gln Gly Gly Cys Ser Ser Ile  
 500 505 510  
 Leu Gly Asn Ser Lys His Lys Ala Pro Leu Ser Gly Pro His Ile Asn  
 515 520 525  
 Ala Ile Thr Glu Glu Lys Gly Ser Ile Leu Ile Ser Trp Asn Ser Ile  
 530 535 540  
 Pro Val Gln Glu Gln Met Gly Cys Leu Leu His Tyr Arg Ile Tyr Trp  
 545 550 555 560  
 Lys Glu Arg Asp Ser Asn Ser Gln Pro Gln Leu Cys Glu Ile Pro Tyr  
 565 570 575  
 Arg Val Ser Gln Asn Ser His Pro Ile Asn Ser Leu Gln Pro Arg Val  
 580 585 590  
 Thr Tyr Val Leu Trp Met Thr Ala Leu Thr Ala Ala Gly Glu Ser Ser  
 595 600 605  
 His Gly Asn Glu Arg Glu Phe Cys Leu Gln Gly Lys Ala Asn Trp Met  
 610 615 620  
 Ala Phe Val Ala Pro Ser Ile Cys Ile Ala Ile Ile Met Val Gly Ile  
 625 630 635 640  
 Phe Ser Thr His Tyr Phe Gln Gln Lys Val Phe Val Leu Leu Ala Ala  
 645 650 655  
 Leu Arg Pro Gln Trp Cys Ser Arg Glu Ile Pro Asp Pro Ala Asn Ser  
 660 665 670  
 Thr Cys Ala Lys Lys Tyr Pro Ile Ala Glu Glu Lys Thr Gln Leu Pro  
 675 680 685  
 Leu Asp Arg Leu Leu Ile Asp Trp Pro Thr Pro Glu Asp Pro Glu Pro  
 690 695 700  
 Leu Val Ile Ser Glu Val Leu His Gln Val Thr Pro Val Phe Arg His  
 705 710 715 720  
 Pro Pro Cys Ser Asn Trp Pro Gln Arg Glu Lys Gly Ile Gln Gly His  
 725 730 735

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Gln Ala Ser Glu Lys Asp Met Met His Ser Ala Ser Ser Pro Pro Pro  
740 745 750

Pro Arg Ala Leu Gln Ala Glu Ser Arg Gln Leu Val Asp Leu Tyr Lys  
755 760 765

Val Leu Glu Ser Arg Gly Ser Asp Pro Lys Pro Glu Asn Pro Ala Cys  
770 775 780

Pro Trp Thr Val Leu Pro Ala Gly Asp Leu Pro Thr His Asp Gly Tyr  
785 790 795 800

Leu Pro Ser Asn Ile Asp Asp Leu Pro Ser His Glu Ala Pro Leu Ala  
805 810 815

Asp Ser Leu Glu Glu Leu Glu Pro Gln His Ile Ser Leu Ser Val Phe  
820 825 830

Pro Ser Ser Ser Leu His Pro Leu Thr Phe Ser Cys Gly Asp Lys Leu  
835 840 845

Thr Leu Asp Gln Leu Lys Met Arg Cys Asp Ser Leu Met Leu  
850 855 860